AMENDMENTS TO THE CLAIMS

Listing of Claims

This listing of the claims will replace all prior versions, and listings, of claims in this application.

1 – 59. (**Cancelled**)

60. (**Currently Amended**) A method of identifying compounds that bind to a leukotriene A_4 (LTA_4) hydrolase comprising the amino acid sequence of SEQ ID NO:1, the method comprising the steps of:

(a) crystallizing a purified LTA_4 hydrolase comprising the amino acid sequence of SEQ ID NO:1 together with bestatin to form an LTA_4 hydrolase crystal;

(b) determining the atomic coordinates of said LTA_4 hydrolase crystal; and

(c) screening the atomic coordinates of a set of candidate compounds against the atomic coordinates of said LTA_4 hydrolase crystal obtained in step a) to identify compounds that bind to the LTA_4 hydrolase.

61. (**Previously Presented**) The method of claim 60, wherein the LTA_4 hydrolase is purified by adsorption chromatography on hydroxyapatite and anion-exchange chromatography.

62. (**Currently Amended**) The method of claim 60, wherein the purified LTA_4 hydrolase is crystallized using $YbCl_3$ as an additive ~~and a complementary compound as a complexing agent~~.

63-67. (**Cancelled**)

68. (**Previously Presented**) The method of claim 60, wherein the atomic coordinates of said LTA_4 hydrolase crystal correspond to the atomic coordinates defining atom 1 to atom 4876 as set forth in Table 9.

69. (**Cancelled**)

70. (**Currently Amended**) A method of designing an inhibitor or agonist of LTA_4 hydrolase comprising the amino acid sequence of SEQ ID NO:1, the method comprising the steps of:

(a) crystallizing a purified LTA_4 hydrolase comprising the amino acid sequence of SEQ ID NO:1 together with bestatin to form a crystal and thereafter determining its conformational structure;

(b) identifying ~~and/ or synthesizing~~ at least one compound that is at least in part complementary to the LTA_4 hydrolase by the use of the conformational structure of the crystal complex obtained in step a); ~~binds to LTA_4 hydrolase by screening the atomic coordinates of a set of candidate compounds against the atomic coordinates of a purified LTA_4 hydrolase crystal;~~

~~(b) refining the compound identified and/ or synthesized by step (a) by cycles of X-ray crystallography; and~~

(c) soaking the crystallized LTA_4 hydrolase obtained in step a) with a solution of a compound identified in step b) to obtain a complex of the crystal of said LTA4 hydrolase and said compound; and~~evaluating the bioactivity of the identified and/or synthesized compound by assessing the activity of LTA_4 hydrolase.~~

(d) performing X-ray crystallography of the crystal complex of LTA_4 hydrolase and said compound to determine the structure thereof, thereby identifying the compound as an inhibitor or agonist of LTA_4 hydrolase.

71. (**Previously Presented**) The method of claim 70, wherein the LTA_4 hydrolase is purified by adsorption chromatography on hydroxyapatite and anion-exchange chromatography.

72. (**Previously Presented**) The method of claim 70, wherein said compound is an inhibitor of LTA_4 hydrolase.

73-75. (**Cancelled**)

76. (**Previously Presented**) The method of claim 70, wherein the atomic coordinates of said LTA_4 hydrolase crystal correspond to the atomic coordinates defining atom 1 to atom 4876 as set for in Table 9.

77. (**Cancelled**)

78. (**New**) The method of claim 70, further comprising the step of refining the structure of said compound obtained in step d) via computer modeling using data obtained from the X-ray crystallography in step d) and repeating steps b)-d).

79. (**New**) The method of claim 70, wherein the complex obtained in step c) comprises bestatin.

80. (**New**) A method of identifying compounds that bind to a leukotriene A_4 (LTA_4) hydrolase comprising an amino acid sequence of at least 90% identity to the amino acid sequence of SEQ ID NO:1, the method comprising the steps of:

(a) crystallizing a purified LTA_4 hydrolase comprising an amino acid sequence of at least 90% identity to the amino acid sequence of SEQ ID NO:1 together with bestatin to form an LTA_4 hydrolase crystal;

(b) determining the atomic coordinates of said LTA_4 hydrolase crystal; and

(c) screening the atomic coordinates of a set of candidate compounds against the atomic coordinates of said LTA_4 hydrolase crystal obtained in step a) to identify compounds that bind to the LTA_4 hydrolase.

81. (**New**) The method of claim 80, wherein the LTA_4 hydrolase comprises an enzymatically active site defined by the following amino acids: Gln136; Ala 137; Tyr267; Gly268; Gly269; Met270; Glu271; Val292; His295; Glu296; His299; Trp315; Glu318; Val322; Phe362; Val367; Leu369; Pro374; Asp375; lle372; Ala377; Pro382; Tyr378; Tyr383; Arg563; and Lys565 of SEQ ID NO:1.

82. (**New**) The method of claim 80, wherein the LTA_4 hydrolase comprises an enzymatically active site defined by the following amino acids: Gln136; Ala137; Tyr267; Gly268; Gly269; Met270; Glu271; Val292; His295; Glu296; His299; Glu318; Tyr378; Tyr383; Arg563; and Lys565 of SEQ ID NO:1.

83. (**New**) A method of designing an inhibitor or agonist of an LTA_4 hydrolase comprising an amino acid sequence of at least 90% identity to the amino acid sequence of SEQ ID NO:1, the method comprising the steps of:

(a) crystallizing a purified LTA_4 hydrolase comprising an amino acid sequence of at least 90% identity to the amino acid sequence of SEQ ID NO:1 together with bestatin to form a crystal and thereafter determining its conformational structure;

(b) identifying at least one compound that is at least in part complementary to the LTA_4 hydrolase by the use of the conformational structure of the crystal complex obtained in step a);

(c) soaking the crystallized LTA_4 hydrolase obtained in step a) with a solution of a compound identified in step b) to obtain a complex of the crystal of said LTA4 hydrolase and said compound; and

(d) performing X-ray crystallography of the crystal complex of LTA_4 hydrolase and said compound to determine the structure thereof, thereby identifying the compound as an inhibitor or agonist of the LTA_4 hydrolase.

84. (**New**) The method of claim 83, wherein the LTA_4 hydrolase comprises an enzymatically active site defined by the following amino acids: Gln136; Ala 137; Tyr267; Gly268; Gly269; Met270; Glu271; Val292; His295; Glu296; His299; Trp315; Glu318; Val322; Phe362; Val367; Leu369; Pro374; Asp375; lle372; Ala377; Pro382; Tyr378; Tyr383; Arg563; and Lys565 of SEQ ID NO:1.

85. (**New**) The method of claim 83, wherein the LTA_4 hydrolase comprises an enzymatically active site defined by the following amino acids: Gln136; Ala137; Tyr267; Gly268; Gly269; Met270; Glu271; Val292; His295; Glu296; His299; Glu318; Tyr378; Tyr383; Arg563; and Lys565 of SEQ ID NO:1.

86. (**New**) The method of claim 83, further comprising the step of refining the structure of said compound obtained in step d) via computer modeling using data obtained from the X-ray crystallography in step d) and repeating steps b)-d).